



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Seed, Brian et al.
- (ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES AND METHODS
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Clark & Elbing LLP  
(B) STREET: 585 Commercial Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02109-1024
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patent in Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/756,018  
(B) FILING DATE: 25-NOV-96  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/661,960  
(B) FILING DATE: 12-JUN-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/000,213  
(B) FILING DATE: 14-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Elbing, Karen Lech  
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(C) REFERENCE/DOCKET NUMBER: 00786/284002
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617/723-6777  
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(C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro  
1 5 10 15

Val Thr

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro  
1 5 10 15

Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp  
20 25 30

Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro  
35 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe  
1 5 10 15

Leu Pro Glu Thr  
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asp Arg Arg Gln Ala Thr Glu Phe Glu Phe Leu Asp Phe Asp Phe  
1 5 10 15

Leu Pro Glu Thr  
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Arg Arg Gln Ala Ala Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe  
1 5 10 15

Leu Pro Glu Ala  
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

00000" 03095'80

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Asp Arg Arg Gln Ala Ala Glu Phe Glu Phe Leu Asp Phe Asp Phe  
 1 5 10 15

Leu Pro Glu Ala  
 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2287 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCTCTTCT TTGTGGTGGC AGCAGCTACA 60  
 GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGGCTG AGGTGAAGAA GCCTGGGTCC 120  
 TCGGTGAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG 180  
 GTGCGACAGG CCCCTGGACA AGGGCTTGAG TCGATGGGAG GGATCATCCC TATCTTTGGT 240  
 ACAGCAAACCT ACGCACAGAA GTTCCAGGTC AGAGTCACGA TTACCGCGGA CGAATCCACG 300  
 AGCACAGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT 360  
 GCGAGAGATA ATGGAGCGTA TTGTAGTGGT GGTAGCTGCT ACTCGGGCTG GTTCGACCCC 420  
 TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATTCT AGCTTTCTGG 480  
 GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC 540  
 GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC 600  
 AGTTAAGAAC CCAGGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCACACACC GCGGTCACAT 660  
 GGCACCACCT CTCTTGCAGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC 720  
 TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTAATTCCCC 780

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GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCCG	840
GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC	900
AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG	960
GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC	1020
AGCGCTCCTG CCTGGACGCA TCCCGGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC	1080
CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT	1140
TCTGGCTTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACC CAGGCCCTGC	1200
ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC	1260
CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT	1320
CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT CTTGTGACAA	1380
AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCGAG GCCTCGCCCT CCAGCTCAAG	1440
GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCAGCCG GGTGCTGACA	1500
CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT	1560
TCCCCCAA AACCAGGAC ACCCTCATGA TCTCCCGGAG CCCTGAGGTC ACATGCGTGG	1620
TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG	1680
AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG	1740
TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC AAGTGCAAGG	1800
TCTCCAACAA AGCCCTCCCA GCCCCATCG AGAAACCAT CTCCAAAGCC AAAGGTGGGA	1860
CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA	1920
GTGACCGCTG TACCAACCTC TGTCCTACAG GGCAGCCCCG AGAACCACAG GTGTACACCC	1980
TGCCCCATC CCGGGATGAG CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG	2040
GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGCGCAGCCG GAGAACAAC	2100
ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAAGCTCA	2160
CCGTGGACAA GAGCAGGTGG CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG	2220
CTCTGCACAA CCACTACACG CAGAAGAGCC TCTCCCTGTC TCCGGTAAA TGAGTGCGAC	2280
GGCCGGC	2287

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val  
1 5 10 15  
Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly  
20 25 30  
Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala  
35 40 45  
Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala  
50 55 60  
Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly  
65 70 75 80  
Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala  
85 90 95  
Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser  
100 105 110  
Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr  
115 120 125  
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
130 135 140  
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
145 150 155 160  
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
165 170 175  
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
180 185 190  
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys  
195 200 205  
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
210 215 220

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Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
225 230 235 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
245 250 255

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
260 265 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
275 280 285

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
290 295 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
305 310 315 320

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
340 345 350

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
435 440

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

0356018-032097

ATGGCGCTGT	CCTGGGTTCT	TACAGTCCTG	AGCCTCCTAC	CTCTGCTGGA	AGCCCAGATC	60
CCATTGTGTG	CCAACCTAGT	ACCGGTGCCC	ATCACCAACG	CCACCCTGGA	CCAGATCACT	120
GGCAAGTGGT	TTTATATCGC	ATCGGCCTTT	CGAAACGAGG	AGTACAATAA	GTCGGTTCAG	180
GAGATCCAAG	CAACCTTCTT	TTACTTCACC	CCCAACAAGA	CAGAGGACAC	GATCTTTCTC	240
AGAGAGTACC	AGACCCGACA	GGACCAGTGC	ATCTATAACA	CCACCTACCT	GAATGTCCAG	300
CGGGAAAATG	GGACCATCTC	CAGATACGTG	GGAGGCCAAG	AGCATTTCGC	TCACTTGCTG	360
ATCCTCAGGG	ACACCAAGAC	CTACATGCTT	GCTTTTGACG	TGAACGATGA	GAAGAACTGG	420
GGGCTGTCTG	TCTATGCTGA	CAAGCCAGAG	ACGACCAAGG	AGCAACTGGG	AGAGTTCTAC	480
GAAGCTCTCG	ACTGCTTGCG	CATTCCCAAG	TCAGATGTCG	TGTACACCGA	TTGGAAAAAG	540
GATAAGTGTG	AGCCACTGGA	GAAGCAGCAC	GAGAAGGAGA	GGAAACAGGA	GGAGGGGGAA	600
TCGGATCCCG	AGGGTGAGTA	CTAAGCTTCA	GCGCTCCTGC	CTGGACGCAT	CCCGGCTATG	660
CAGCCCCAGT	CCAGGGCAGC	AAGGCAGGCC	CCGTCTGCCT	CTTCACCCGG	AGCCTCTGCC	720
CGCCCCACTC	ATGCTCAGGG	AGAGGGTCTT	CTGGCTTTTT	CCCAGGCTCT	GGGCAGGCAC	780
AGGCTAGGTG	CCCCTAACCC	AGGCCCTGCA	CACAAAGGGG	CAGGTGCTGG	GCTCAGACCT	840
GCCAAGAGCC	ATATCCGGGA	GGACCCTGCC	CCTGACCTAA	GCCCACCCCA	AAGGCCAAAC	900
TCTCCACTCC	CTCAGCTCGG	ACACCTTCTC	TCCTCCCAGA	TTCCAGTAAC	TCCCAATCTT	960
CTCTCTGCAG	AGCCCCAAATC	TTGTGACAAA	ACTCAGCAT	GCCCACCGTG	CCCAGGTAAG	1020
CCAGCCCAGG	CCTCGCCCTC	CAGCTCAAGG	CGGGACAGGT	GCCCTAGAGT	AGCCTGCATC	1080
CAGGGACAGG	CCCCAGCCGG	GTGCTGACAC	GTCCACCTGC	ATCTCTTCCT	CAGCACCTGA	1140
ACTCCTGGGG	GGACCGTCAG	TCTTCCTCTT	CCCCCAAAA	CCCAAGGACA	CCCTCATGAT	1200
CTCCCGGACC	CCTGAGGTCA	CATGCGTGGT	GGTGGACGTG	AGCCACGAAG	ACCCTGAGGT	1260
CAAGTTCAAC	TGGTACGTGG	ACGGCGTGGA	GGTGCATAAT	GCCAAGACAA	AGCCGCGGGA	1320
GGAGCAGTAC	AACAGCACGT	ACCGGGTGGT	CAGCGTCCTC	ACCGTCCTGC	ACCAGGACTG	1380
GCTGAATGGC	AAGGAGTACA	AGTGCAAGGT	CTCCAACAA	GCCCTCCCAG	CCCCCATCGA	1440
GAAAACCATC	TCCAAAGCCA	AAGGTGGGAC	CCGTGGGGTG	CGAGGGCCAC	ATGGACAGAG	1500
GCCGGCTCGG	CCCACCTCT	GCCCTGAGAG	TGACCGCTGT	ACCAACCTCT	GTCTACAGG	1560
GCAGCCCCGA	GAACCACAGG	TGTACACCCT	GCCCCCATCC	CGGGATGAGC	TGACCAAGAA	1620



CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC AGCGACATCG CCGTGGAGTG 1680  
GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA 1740  
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGGAA 1800  
CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC AGAAGAGCCT 1860  
CTCCCTGTCT CCGGGTAAAT GAGTGCGACG GCCG 1894

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Leu	Ser	Trp	Val	Leu	Thr	Val	Leu	Ser	Leu	Leu	Pro	Leu	Leu
1				5					10					15	
Glu	Ala	Gln	Ile	Pro	Leu	Cys	Ala	Asn	Leu	Val	Pro	Val	Pro	Ile	Thr
			20					25					30		
Asn	Ala	Thr	Leu	Asp	Gln	Ile	Thr	Gly	Lys	Trp	Phe	Tyr	Ile	Ala	Ser
			35					40				45			
Ala	Phe	Arg	Asn	Glu	Glu	Tyr	Asn	Lys	Ser	Val	Gln	Glu	Ile	Gln	Ala
			50			55					60				

Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu	65	70	75	80
Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr	85	90	95	
Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly	100	105	110	
Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr	115	120	125	
Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val	130	135	140	
Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr	145	150	155	160
Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp Val Val Tyr Thr	165	170	175	
Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys Gln His Glu Lys	180	185	190	
Glu Arg Lys Gln Glu Glu Gly Glu Ser Asp Pro Glu Gly Glu Pro Lys	195	200	205	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	210	215	220	
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	225	230	235	240
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	245	250	255	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	260	265	270	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	275	280	285	
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	290	295	300	
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	305	310	315	320
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	325	330	335	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln	340	345	350	

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 420 425 430

Leu Ser Pro Gly Lys  
 435

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 442 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val  
 1 5 10 15

Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly  
 20 25 30

Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala  
 35 40 45

Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala  
 50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly  
 65 70 75 80

Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala  
 85 90 95

Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser  
 100 105 110

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Cys Tyr Ser Gly Trp Phe Asp	Pro Trp Gly Gln Gly Thr Leu Val Thr
115	120 125
Val Ser Ser Ala Ser Thr Lys	Gly Pro Ser Val Phe Pro Leu Ala Pro
130	135 140
Ser Ser Lys Ser Thr Ser Gly	Gly Thr Ala Ala Leu Gly Cys Leu Val
145	150 155 160
Lys Asp Tyr Phe Pro Glu Pro Val	Thr Val Ser Trp Asn Ser Gly Ala
165	170 175
Leu Thr Ser Gly Val His Thr Phe	Pro Ala Val Leu Gln Ser Ser Gly
180	185 190
Leu Tyr Ser Leu Ser Ser Val Val	Thr Val Pro Ser Ser Ser Asp Lys
195	200 205
Lys Val Glu Pro Lys Ser Cys Asp	Lys Thr His Thr Cys Pro Pro Cys
210	215 220
Pro Ala Pro Glu Leu Leu Gly Gly	Pro Ser Val Phe Leu Phe Pro Pro
225	230 235 240
Lys Pro Lys Asp Thr Leu Met Ile Ser	Arg Thr Pro Glu Val Thr Cys
245	250 255
Val Val Val Asp Val Ser His Glu Asp	Pro Glu Val Asn Phe Ser Trp
260	265 270
Tyr Val Asp Gly Val Glu Val His Asn	Asn Lys Thr Lys Pro Arg Glu
275	280 285
Glu Asn Tyr Ser Ser Thr Tyr Arg	Val Val Ser Val Leu Thr Val Leu
290	295 300
His Gln Asp Trp Leu Asn Gly Lys	Glu Tyr Lys Cys Asn Val Ser Asn
305	310 315 320
Lys Ala Leu Pro Ala Pro Ile Glu	Lys Asn Ile Ser Lys Ala Lys Gly
325	330 335
Gln Pro Arg Glu Pro Gln Val Tyr Thr	Leu Pro Pro Ser Arg Asp Glu
340	345 350
Leu Thr Lys Asn Gln Val Ser Leu Thr	Cys Leu Val Lys Gly Phe Tyr
355	360 365
Pro Ser Asp Ile Ala Val Glu Trp	Glu Ser Asn Gly Gln Pro Glu Asn
370	375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly  
 1 5 10 15

Pro Gly Thr Pro Glu Ser Thr Thr Val Glu Pro Ala Ala Arg Arg Ser  
 20 25 30

Thr Gly Leu Asp Ala Gly Gly Ala Val Thr Glu  
 35 40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser Thr Asp Ser Ala  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asp Tyr Glu Tyr Asp Glu Leu Pro  
1                      5

260220" 8T095280